

## Analysis of genetic components of variance and other quantitative characters in a high lysine maize, DQPMC-4(W) composite at two plant densities

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**ABSTRACT:** DQPMC(W)-4, an open-pollinated variety was used as an experimental material. Biparental progenies were developed using NC Design-I. Fourteen quantitative traits were measured in 128 full-sibs and 32 S1 randomly developed families derived from the maize population, DQPMC-4(W) which were grown in randomized block design at normal and high plant densities. Components of variance, genetic components of variance, degree of dominance, heritability and expected genetic gains from selection were estimated for each trait. Results obtained from the present investigation revealed that sources of variations differed significantly for most of the traits at both normal and high plant densities. Combined analysis over both the environments also depicted significant differences among source of variations for most of the traits. On the basis of expectation of mean squares, estimates of variances due to males ( $\sigma^2_m$ ) and females ( $\sigma^2_f$ ) were calculated along with their standard errors which showed that variances due to males and females were found to be significant for most of the traits at normal and high plant densities. Negative estimates of  $\sigma^2_m$  and  $\sigma^2_f$  were also recorded for some traits. Estimates of genetic components of variance revealed greater importance of additive genetic variance ( $\sigma^2_A$ ) as compared to dominance genetic variance ( $\sigma^2_D$ ) for most of the traits at both the plant densities. General mean, heritability and expected genetic gain studied at high plant density were found to be higher than normal plant density. Since, there was preponderance of additive genetic variance for most of the characters studied; further improvement can be made in this population through intra-population recurrent selection procedure.

**Key words:** Additive genetic variance, genetic gain, heritability, maize, North Carolina Design 1, *Zea mays*

Maize (*Zea mays* L.) being a major cereal crop is used for human nutrition, animal feed and fodder and various industrial products (starch, oil, glucose, alcohol, ethanol etc.), worldwide. Maize is reputed as a nutria-cereal because of its high contents of carbohydrates, fats, proteins, some of the important vitamins and minerals. In many of the developing countries, several millions of people derive their protein and calorie requirements from maize.

QPM breeding began with the objective of improving the nutritional value of maize grain protein. *Opaque-2* maize, however, have limited its wide-spread cultivation because of having many agronomic deficiencies associated with it. Genetic improvement of economically important traits along with maintaining sufficient variability is always the desired objective in maize breeding programmes (Hallauer, 1978). Greater the variability, more are the chances of getting desired types. Estimates of genetic, environmental and genetic-environment interaction components of variance are obtained from the appropriate analysis of variance for the mating designs used in developing progenies (Cockerham, 1963). Precision of the

estimates depends on adequate sampling of the population of genotypes and environments. Information regarding various components of genetic variance is very useful for plant breeders as a guide in choosing an appropriate breeding method.

Most of the studies based on the estimation of genetic variances have been based on single plant population density. Therefore, studies of estimation of genetic variances under different plant population densities are required to provide information regarding differences in genetic and phenotypic variances and genotypes by density interaction. The objective of the present investigation was to obtain estimates of genetic parameters involving fourteen characters under different plant population densities and examine the suitability of the population for exploitation through population improvement and hybrid breeding as well.

### MATERIALS AND METHODS

For the present investigation DQPMC-4(W), an open-pollinated variety was used as an experimental

material. North Carolina Design I (NCD-I) was undertaken for developing biparental progenies as given by Comstock and Robinson (1948, 1952). The base population, DQPMC-4(W) was planted during *Rabi, 2009-10* to initiate development of progenies at N. E. Borlaug Crop Research Centre, G.B.P.U.A. &T., Pantnagar. Thirty two plants from base population were selected and were considered as males. Each of male plant was crossed with four randomly selected female plants within the same population and each male parent was simultaneously selfed to produce  $S_1$  families. Since, the group of four progenies involving the same male forms a male group, therefore, there were thirty two such male groups. As a result, a total of 128 progenies were developed within the population. A set was constituted by four male groups, thus there were eight sets in total. No female was involved in more than one mating.

The resulting 32  $S_1$  families and 128 full sib families were grown in two environments of normal (53,333 plants/ha) and high (66,666 plants/ha) plant densities in randomized block design with three replications during *Kharif, 2010 A* total of fourteen characters were observed during the experiment. In respect of days to 50 per cent tasselling, days to 50 per cent silking and grain yield data were recorded on the whole plot basis, whereas plant height, ear height, ear length, ear diameter, number of kernel rows/ear, number of kernels/row and moisture % at harvest were recorded on the basis of five randomly selected competitive plants. By compositing the seeds of 5 randomly selected plants from a plot of biparental families at normal and high plant densities, 100-kernel weight, protein (%), tryptophan (g/16g N) and lysine (g/16g N) were calculated. Protein was chemically analyzed using the procedure of Micro-Kjeldahl as described in the A.O.A.C. (1965) and tryptophan and lysine content was estimated by using the protocol of Hernandez and Bates (1969) for the evaluation of opaque-2 maize materials.

The obtained values were submitted for further statistical analysis.

## RESULTS AND DISCUSSION

Results obtained from the present investigation revealed that sources of variations differed significantly for most of the traits at both normal and high plant densities (Table 1, 2). The mean sum of squares due to replication was highly significant for protein, tryptophan and lysine contents in case of normal plant density, while

in high plant density; it was highly significant for days to 50 per cent tasselling and significant for ear length, number of kernels/ row, moisture per cent at harvest and lysine. Variance due to sets was highly significant for all the characters except plant height and ear diameter at normal plant density. Similarly, it was significant for all the traits except ear diameter at high plant density. The mean sum of squares due to sets  $\times$  replications was highly significant for protein per cent, tryptophan and lysine contents at normal plant density, while at high plant density it was highly significant for days to 50 per cent tasselling, ear height, moisture % at harvest, protein per cent and significant for tryptophan and lysine contents. The mean sum of squares due to males/set was highly significant for all the characters at both normal as well as high plant densities except ear diameter which was significant at normal plant density.

The mean sum of squares due to females/males/sets was highly significant for all the characters except ear diameter at normal plant density and ear diameter and number of kernel rows/ear at high plant density. Combined analysis (Table 3) over both the environments also depicted significant differences among source of variations for most of the traits. In combined analysis, the mean sum of squares due to environment was highly significant for all the characters except number of kernel rows/ear, and protein per cent. Variance due to replications/environment was highly significant for days to 50 percent tasselling, ear height, protein percent, tryptophan and lysine contents and significant for number of kernel rows/ear. The mean sum of squares due to sets/replications/environment was highly significant for all the characters except ear diameter. The mean sum of squares due to males/sets was highly significant for plant height, ear diameter, number of kernel rows/ear, protein per cent, tryptophan and lysine contents. The mean sum of squares due to females/sets was highly significant for plant height, number of kernel rows/ear, moisture % at harvest, protein per cent, tryptophan, lysine contents and significant for days to 50 per cent silking, ear length and number of kernels/row. Variance due to environment  $\times$  males/sets and environment  $\times$  females/males/sets was significant for all the characters except number of kernel rows/ear in environment  $\times$  males/sets whereas ear diameter and number of kernel rows/ear for environment  $\times$  females/males/sets.

These results were in agreement with the results obtained by Gozubenli, H. (2010). In his studies he observed that grain yield and yield related traits of maize

Table 1: Analysis of variance of NCD-I progenies for important economic characters in quality protein maize at normal plant density

Source of variations	Mean squares														
	d.f.	Days to tasselling	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Number of kernels/rows/ear	Number of kernels/ear	100 kernels weight	Grain yield	Moisture % at harvest	proetin	Trypto-phan	lysine
Replications	2	1.96	4.46	6.23	12.32	0.09	0.21	4.12	0.92	0.62	2.63	7.23	4.26**	0.045**	0.59**
Sets	7	34.12**	31.25**	271.56	143.27**	4.21**	0.32	6.32**	25.44**	9.57**	312.25**	142.92**	15.23**	0.092**	2.96**
Sets×replications	14	2.56	2.14	198.52	11.25	1.03	0.43	3.25	2.96	2.13	2.35	4.76	2.53**	0.054**	0.42**
Males/sets	24	12.34**	10.04**	435.59**	153.23**	7.54**	0.53*	7.45**	41.23**	10.53**	96.35**	69.46**	10.23**	0.099**	2.53**
Females/males/sets	96	3.12**	3.06**	199.63*	35.27**	2.89**	0.41	3.56**	12.03**	3.43**	26.53**	56.74**	4.23**	0.042**	0.62**
Pooled error	254	2.04	1.98	185.45	10.05	1.12	0.23	2.38	2.45	2.89	2.48	1.84	0.56	0.009	0.08
Total		3.56	3.12	211.36	29.89	2.15	0.31	2.89	7.56	2.99	20.13	7.53	2.12	0.09	0.58

\*, \*\* Significant at 5 and 1 % probability levels, respectively

Table 2: Analysis of variance of NCD-I progenies for important economic characters in quality protein maize at high plant density

Source of variations	Mean squares														
	d.f.	Days to tasselling	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Number of kernels/rows/ear	Number of kernels/ear	100 kernels weight	Grain yield	Moisture % at harvest	proetin	Trypto-phan	lysine
Replications	2	36.53**	2.27	34.53	7.89	4.98*	0.45	3.98	7.23*	0.75	1.25	6.95*	0.96	0.009	0.24*
Sets	7	36.12**	11.23**	483.43**	715.56**	10.25**	0.49	4.56**	61.23**	5.23**	205.2**	136.55**	14.23**	0.099**	1.24**
Sets×replications	14	2.98**	1.26	10.23	21.26**	0.98	0.29	2.59	2.14	1.96	1.99	2.76**	1.53**	0.009*	0.09*
Males/sets	24	10.25**	14.26**	669.34**	134.85**	4.56**	0.65**	5.86**	54.23**	11.56**	315.23**	135.26**	10.96**	0.12**	1.89**
Females/males/sets	96	2.32**	3.45**	212.23**	32.23**	2.12**	0.39	2.98	13.03**	3.53**	92.53**	61.70**	2.53**	0.026**	0.56**
Pooled error	254	1.56	2.13	13.56	10.25	1.58	0.32	1.13	2.53	1.59	1.24	1.92	0.89	0.005	0.09
Total		3.02	3.58	113.59	34.56	2.10	0.28	2.53	10.26	2.18	39.58	6.53	2.14	0.06	0.48

\*, \*\* Significant at 5 and 1 % probability levels, respectively

Table 3: Analysis of variance of NCD-I progenies for important economic characters in quality protein maize in combined analysis

Source of variations	Mean squares														
	d.f.	Days to tasselling	Days to 50% silking	Plant height	Ear height	Ear length	Ear diameter	Number of kernels/rows/ear	Number of kernels/ear	100 kernels weight	Grain yield	Moisture % at harvest	Proetin	Trypto-phan	lysine
Environment (E)	1	46.23**	185.35**	9568.42**	3425.18**	16.45**	2.78**	2.41	201.51**	29.03**	1243.59**	182.94**	0.48	0.09*	1.29**
Replications/E	4	24.53**	5.26	26.34	11.26**	4.09	0.89	6.58*	5.79	0.99	2.85	62.54	4.23**	0.09**	0.96**
Sets/replications/E	42	19.56**	10.53**	211.31**	196.57**	5.03**	0.84	5.23**	16.59**	4.59**	92.56**	41.23**	7.12**	0.11**	1.20**
Males/sets	24	16.23	19.58	1023.56**	211.43	7.13	0.61**	12.03**	53.21	15.64	145.55	119.5	24.12**	0.95**	3.44**
Females/males/sets	96	4.89	6.92*	412.58**	61.23	4.05*	0.46	6.53**	24.53**	4.86	56.23	46.59**	6.29**	0.04**	0.66**
E×males/sets	24	8.53**	9.19**	346.28**	110.26**	6.59**	0.89*	109.56	64.48**	9.65**	245.62**	72.02**	113.51**	0.09**	0.46**
E×females/males/sets	96	4.34**	4.12**	156.27*	64.23**	2.46*	0.95	0.98	10.43**	4.56**	56.23**	49.37**	1.16**	0.045**	0.99*
Pooled error	30	3.11	2.48	106.5	11.23	112.03	0.34	2.46	3.46	3.12	106.53	0.88	0.62	0.002	0.08
Total	767	4.65	4.53	316.01	64.23	2.89	0.49	2.98	9.16	5.11	54.16	27.74	2.49	0.06	0.83

\*, \*\* Significant at 5 and 1 % probability levels, respectively

except for tasselling period were significantly affected by plant densities. On the basis of expectation of mean squares, estimates of variances due to males ( $\sigma_m^2$ ) and females ( $\sigma_f^2$ ) were calculated along with their standard errors (Table 4) which showed variances due to males and females were found to be significant for most of the traits at normal and high plant densities. The values of variances due to males ( $38.09 \pm 15.68$ ) and variances due to females ( $66.22 \pm 10.11$ ) were observed to be highest for plant height at high plant density. Similarly these values were also found to be highest (i.e. the estimates of variances due to males and females,  $70.16 \pm 12.76$  &  $42.71 \pm 10.5$ , respectively) for plant height in combined analysis. The estimates of variances due to males x plant densities interactions ( $15.83 \pm 8.21$ ) and females x plant densities interactions ( $16.59 \pm 11.58$ ) also revealed highest values for plant height in combined analysis. While these estimates were lowest for tryptophan content at both normal as well as high plant densities. Negative estimates of  $\sigma_m^2$  and  $\sigma_f^2$  were also recorded for some traits which may be due to lack of random mating and/or inadequate sampling while making half-sib groups. Similar results have been obtained by Lindsey *et al.* (1962). He reported that negative estimates may result from sampling error in estimating a value which was either zero or very small positive. Higher magnitude of variance due to females as compared to variances due to males for most of the traits in both the plant densities indicated that both additive as well as dominance variance made the contribution towards genetic variability.

Estimates of genetic components of variance revealed greater importance of additive genetic variance ( $\sigma_a^2$ ) as compared to dominance genetic variance ( $\sigma_b^2$ ) for most of the traits at both the plant densities (Table 5). Alves *et al.* (2002), Raposo and Ramalho (2004) and Revilla *et al.* (2004) also found the similar results in their experiments. In contrast there are various studies which revealed greater importance of dominance variance as compared to additive variance (Irshad-Ul-Haq, 2010 and M. El-Badawy, 2011). Negative estimates of additive and dominance variances were also observed. The negative estimates obtained in the present study were well within the range possible through sampling error, assuming that true dominance variance was small and not significantly different from zero. Combined analysis over both the environments indicated that both additive and dominance variances were significantly interacted with the environments suggesting major role of additive genetic

variance, while dominance  $\times$  plant density interaction variance component played very little role in determining the total genetic variability. Mean, range, coefficient of variability and heritability for all the traits were studied at both normal as well as high plant densities and combined analysis over both the environments was also done (Table 6). General mean for most of the traits like plant and ear heights, ear length, ear diameter, number of kernel rows/ear, number of kernels/row, moisture % at harvest, tryptophan and lysine contents studied at high plant density was found to be higher than normal plant density. Full-sib progeny means showed wider range at normal plant density as compared to high plant density for all traits except plant height, ear height, ear length, ear diameter and moisture % at harvest. In estimating the heritability, variances of males and females were used, although, female variances were less than male variances. It is quite logical to consider specific negative estimate to be very low or close to zero. Thus, its positive counterpart would be considered as sole contributor to total genetic variability observed for the trait. The heritability estimates were higher at high plant density for all the characters studied except ear height, ear length, number of kernel rows/ear, 100-kernel weight, grain yield and lysine content. Nawar *et al.* (1995) estimated heritability values in Giza2 maize population. They found that estimates of heritability were (46%) for number of rows/ear, (5%) for number of kernels/row (13%) for 100-kernel weight, (37%) for ear length, (11%) for ear diameter, (21%) for plant height, (43%) for ear height, (96%) for days to tasselling, (46%) for days to silking. Barakat (2003) studied genetic variance for grain yield and other valuable traits in Gemmeiza yellow maize population. He found that estimates of heritability for all the studied traits were high.

Highest expected genetic gain for lysine content was 76.34 per cent of mean by full-sib family selection (Table 7). Expected genetic gain was more at high plant density than normal plant density for all the characters except days to 50 per cent tasselling, ear height, ear length, number of kernel rows/ear and grain yield indicating that these traits may be used as selection criterion in breeding programmes. Srivastava (2001) reported higher expected genetic advance for grain yield, plant height, ear height and 1000-kernel weight, while moderate values for days to 50 per cent silking, ear length, shelling percentage and number of kernels/row. Low estimates of expected genetic gain were observed by ear width and number of kernel rows/ear.

**Table 4: Variances for yield and its component traits in maize**

Character	Plant density	Variance due to males ( $\sigma_m^2$ )	Variance due to females ( $\sigma_f^2$ )	$\sigma_{me}^2$	$\sigma_{fe}^2$	Variance due to error ( $\sigma_e^2$ )
Days to 50% tasselling	Normal	0.76* ± 0.28	0.36* ± 0.15			2.04 ± 0.18
	High	0.66* ± 0.23	0.25 ± 0.12			1.56 ± 0.14
	Combined	0.41* ± 0.22	0.09 ± 0.15	0.34* ± 0.20	0.41* ± 0.33	3.11 ± 0.78
Days to 50% silking	Normal	0.58* ± 0.23	0.36* ± 0.15			1.98 ± 0.17
	High	0.90* ± 0.33	0.44* ± 0.18			2.13 ± 0.19
	Combined	1.26** ± 0.25	0.47* ± 0.19	0.42* ± 0.21	0.14 ± 0.28	2.48 ± 0.62
Plant height	Normal	19.66* ± 10.34	4.72 ± 10.96			185.45 ± 16.39
	High	38.09* ± 15.68	66.22* ± 10.11			13.56 ± 1.19
	Combined	70.16** ± 12.76	42.7*1 ± 10.5	15.83* ± 8.21	16.59* ± 11.58	106.5 ± 26.63
Ear height	Normal	9.83* ± 3.56	2.10* ± 1.71			10.05 ± 0.79
	High	8.55* ± 3.14	7.33* ± 1.56			10.25 ± 0.91
	Combined	17.36* ± 2.80	- 0.5 ± 2.11	3.84* ± 2.66	17.67* ± 3.19	11.23 ± 2.81
Ear length	Normal	0.39* ± 0.17	0.59* ± 0.14			1.12 ± 0.10
	High	0.20* ± 0.11	0.18* ± 0.11			1.58 ± 0.14
	Combined	-0.18 ± 0.12	0.27* ± 0.11	0.34* ± 0.15	- 38.25 ± 9.33	112.03 ± 28.01
Ear diameter	Normal	0.01 ± 0.01	0.06 ± 0.06			0.23 ± 0.08
	High	0.02 ± 0.02	0.03* ± 0.001			0.32 ± 0.03
	Combined	0.04* ± 0.01	-0.08 ± 0.008	-0.01 ± 0.021	0.20 ± 0.032	0.34 ± 0.085
Number of kernel rows/ear	Normal	0.32* ± 0.17	0.39* ± 0.18			2.38 ± 0.21
	High	0.24* ± 0.14	0.62* ± 0.15			1.13 ± 0.10
	Combined	-17.18 ± 1.27	70.93* ± 0.16	9.04* ± 2.53	-0.49 ± 0.21	2.46 ± 0.62
Number of kernels/row	Normal	2.43* ± 0.96	3.19* ± 0.57			2.45 ± 0.23
	High	3.43* ± 1.26	3.50* ± 0.62			2.53 ± 0.22
	Combined	-4.22 ± 0.98	2.35* ± 0.63	4.50* ± 1.50	2.32* ± 0.57	3.46 ± 0.87
100 kernel weight	Normal	0.59* ± 0.24	0.18 ± 0.18			2.89 ± 0.26
	High	0.66* ± 0.27	0.65* ± 0.18			1.59 ± 0.14
	Combined	0.94* ± 0.22	0.05 ± 0.16	0.42* ± 0.23	0.48* ± 0.34	3.12 ± 0.78
Grain yield	Normal	5.81* ± 2.24	8.02* ± 1.26			2.48 ± 0.22
	High	18.55* ± 7.36	30.43* ± 4.41			1.24 ± 0.11
	Combined	-16.67 ± 3.33	0.01 ± 1.89	15.78* ± 5.72	-16.77 ± 9.27	106.53 ± 26.63
Moisture % at harvest	Normal	1.06 ± 1.74	18.3* ± 2.70			1.84 ± 0.16
	High	6.13* ± 3.21	19.93* ± 2.94			1.92 ± 0.17
	Combined	8.37* ± 1.66	-0.46 ± 1.62	1.89* ± 1.77	16.16* ± 2.35	0.88 ± 0.22
Protein	Normal	0.5* ± 0.24	1.22* ± 0.20			0.56 ± 0.05
	High	0.70* ± 0.26	0.55* ± 0.12			0.89 ± 0.008
	Combined	-15.75 ± 1.34	0.86* ± 0.15	9.36* ± 2.62	0.18* ± 0.11	0.62 ± 0.16
Tryptophan	Normal	0.00048* ± 0.0002	0.011* ± 0.0002			0.009 ± 0.0008
	High	0.0008 ± 0.0009	0.007* ± 0.00042			0.050 ± 0.0044
	Combined	0.14* ± 0.01	-0.08 ± 0.001	0.04* ± 0.0067	0.014* ± 0.00069	0.056 ± 0.0028
Lysine	Normal	0.16* ± 0.06	0.18* ± 0.0004			0.08 ± 0.0007
	High	0.11* ± 0.04	0.16* ± 0.009			0.09 ± 0.008
	Combined	0.55* ± 0.075	-0.06 ± 0.233	-0.04 ± 0.13	0.30* ± 0.47	0.08 ± 0.02

\*, \*\* Significant at 5 and 1 % levels of significance, respectively

Table 5: Estimates of additive genetic variance ( $\sigma^2_A$ ), dominance variance ( $\sigma^2_D$ ), their interaction with environments, ratio of  $\sigma^2_D/\sigma^2_A$  and average degree of dominance in maize

Character density	Plant	$\sigma^2_A$	$\sigma^2_D$	$\sigma^2_{Ae}$	$\sigma^2_{ADe}$	$\sigma^2_{Ge}$	$\sigma^2_D/\sigma^2_A$	Degree of dominance
Days to 50% tasselling	Normal	3.07* ± 1.12	-1.63 ± 1.27				-0.53	-
	High	2.64* ± 0.92	-1.63 ± 1.03				-0.61	-
Days to 50% silking	Combined	1.64* ± 0.86	-1.28 ± 1.05	1.36* ± 0.81	0.28 ± 1.54	1.64* ± 1.32	-0.78	-
	Normal	2.33* ± 0.92	-0.89 ± 1.09				-0.38	-
Plant height	High	3.60* ± 1.33	-1.84 ± 1.5	1.68* ± 0.84	-1.12 ± 1.4	0.56 ± 1.12	-0.51	-
	Combined	5.04* ± 1.0	-3.16 ± 1.25				-0.62	-
Ear height	Normal	78.65* ± 41.36	-59.75 ± 60.27				-0.76	-
	High	152.37* ± 62.7	112.52* ± 74.61	63.32* ± 32.84	3.04 ± 56.78	66.36* ± 46.32	0.73	0.85
Ear length	Combined	280.64** ± 51.04	-109.8 ± 66.09				-0.39	-
	Normal	39.32* ± 14.24	-30.91 ± 15.79	15.36* ± 10.64	55.32* ± 16.61	70.68* ± 12.76	-0.78	-
Ear diameter	High	34.21* ± 12.56	-4.9 ± 14.02				-0.14	-
	Combined	69.44* ± 11.2	-71.44 ± 14.02				-1.02	-
Number of kernel rows/ear	Normal	1.55* ± 0.68	0.81 ± 0.88				0.52	0.72
	High	0.81* ± 0.43	-0.093 ± 0.62	1.36* ± 0.6	-154.36 ± 37.32	-153 ± 37.32	-0.11	-
Number of kernels/row	Combined	-0.72 ± 0.46	1.8* ± 0.64				-2.50	-
	Normal	0.04 ± 0.04	0.20* ± 0.04				5.0	2.23
100 kernel weight	High	0.09* ± 0.06	0.00065 ± 0.019	-0.02 ± 0.08	0.82* ± 0.13	0.80* ± 0.13	0.0074	0.09
	Combined	0.16* ± 0.05	-0.48 ± 0.016				-3.0	-
Grain yield	Normal	1.29* ± 0.68	0.27 ± 0.99				0.20	0.45
	High	0.96* ± 0.56	1.51* ± 0.81	36.16* ± 10.13	-38.12 ± 10.16	-1.96 ± 0.82	1.57	1.25
Moisture % at harvest	Combined	-68.72 ± 5.096	352.44** ± 5.13				-5.12	-
	Normal	9.73* ± 3.84	3.04 ± 4.46				0.31	0.55
Protein	High	13.73* ± 5.04	0.27 ± 5.61	18.0* ± 5.98	-8.72 ± 6.41	9.28* ± 2.30	0.02	0.14
	Combined	16.88* ± 3.92	26.28* ± 4.67				1.55	1.24
Tryptophan	Normal	2.37* ± 0.96	-1.65 ± 1.20				-0.69	-
	High	2.68* ± 1.08	-0.09 ± 1.28	1.68* ± 0.92	0.24 ± 1.63	1.92* ± 1.35	-0.03	-
Lysine	Combined	3.76* ± 0.86	-3.56 ± 1.07				-0.94	-
	Normal	23.27* ± 8.96	8.79 ± 10.28				0.37	0.61
Days to 50% tasselling	High	74.23* ± 29.44	47.49* ± 34.31	63.12* ± 22.86	-130.2 ± 43.56	-67.08 ± 37.08	0.63	0.79
	Combined	-66.68 ± 13.33	66.68* ± 15.33				-1.0	-
Days to 50% silking	Normal	4.24 ± 6.96	68.96* ± 12.84				16.26	4.03
	High	24.52* ± 12.84	55.19* ± 17.41	7.56 ± 7.06	57.08* ± 11.76	64.64* ± 9.41	2.25	1.50
Plant height	Combined	33.48* ± 6.65	-35.32 ± 9.27				-1.05	-
	Normal	2.0* ± 0.96	2.89 ± 3.13				1.45	1.20
Ear height	High	2.81* ± 1.02	-0.62 ± 1.13				-0.22	-
	Combined	-63.0 ± 5.36	66.44* ± 5.39	37.44* ± 10.48	-36.72 ± 10.48	0.72* ± 0.42	-1.05	-
Ear diameter	Normal	0.0019 ± 0.0088	0.042* ± 0.0009				22.11	4.70
	High	0.0015* ± 0.00035	0.025* ± 0.00039	0.016* ± 0.00027	0.04* ± 0.00029	0.056* ± 0.0028	15.92	3.99
Number of kernel rows/ear	Combined	0.56* ± 0.044	-0.88 ± 0.014				-1.57	-
	Normal	0.64* ± 0.23	0.083 ± 0.023				0.13	0.36
Number of kernels/row	High	0.44* ± 0.18	0.184* ± 0.05	-0.16 ± 0.51	1.36 ± 1.93	1.2* ± 1.86	0.41	0.64
	Combined	2.20* ± 0.3	-2.44 ± 0.94				-1.10	-

\*, \*\* Significant at 5 and 1 % levels of significance, respectively

**Table 6: Mean, Range, CV and Heritability ( $h^2$ ) for different characters in maize**

Character	Plant density	Mean	Range	Coefficient of variability (%)	Heritability (%)
Days to 50 % tasselling	Normal	49.6	43-56	2.56	88.31
	High	49.5	45-54	2.42	102.72
	Combined	49.55		2.49	97.0
Days to 50 % silking	Normal	52.3	46-58	2.72	68.03
	High	51.7	47-56	2.81	92.62
	Combined	52.0		2.76	196.0
Plant height	Normal	160.81	115-206	7.93	38.48
	High	178.5	130-226	4.08	54.72
	Combined	169.66		6.01	126.0
Ear height	Normal	66.7	45-88	4.65	213.03
	High	71.5	50-92	3.78	86.48
	Combined	69.1		4.22	197.0
Ear length	Normal	14.4	10.15-18.56	6.02	44.54
	High	14.96	11.33-18.60	6.46	35.35
	Combined	14.68		6.24	1.20
Ear diameter	Normal	4.35	2.85-5.5	10.87	8.51
	High	4.4	2.73-5.65	10.69	21.28
	Combined	4.38		10.78	114.0
Number of kernel rows/ear	Normal	13.5	10-16	9.38	32.80
	High	14.2	10-16	8.34	26.69
	Combined	3.85		8.86	-24.0
Number of kernels/row	Normal	30.8	18-43.6	5.78	63.93
	High	31.4	20.0-42.5	5.61	83.08
	Combined	31.1		5.40	-115.0
100 kernel weight	Normal	27.5	21-33.89	6.75	65.56
	High	26.72	20.5-32.62	5.92	64.09
	Combined	27.11		6.34	223.0
Grain yield	Normal	0.86	0.48-1.20	4.65	67.36
	High	0.75	0.24-1.16	4.72	60.37
	Combined	0.81		4.69	*
Moisture % at harvest	Normal	20.35	13.5-26.9	6.09	5.65
	High	20.75	14.0-27.5	4.56	30.03
	Combined	20.55		5.33	109.0
Protein	Normal	10.32	8.45-11.85	6.15	36.67
	High	9.07	7.24-10.9	6.02	91.33
	Combined	9.65		6.09	-161.4
Tryptophan	Normal	0.86	0.52-1.12	5.56	0.37
	High	0.88	0.65-1.02	5.40	4.99
	Combined	0.87		5.48	-198.0
Lysine	Normal	3.15	2.08-4.48	6.56	79.6
	High	3.23	2.15-4.15	5.24	61.84
	Combined	3.20		5.90	5.78

\*indicates spurious heritability estimates

**Table 7: Estimates of the expected genetic gain per cycle of selection (as individual plant and percent of mean) with full-sib selection at 5 % intensity in maize**

Character	Plant density	Full-sib selection	
		Individual plant	Percent of mean
Days to 50 % tasselling	Normal	0.147	4.74
	High	0.114	4.59
	Combined	0.063	2.79
Days to 50 % silking	Normal	0.057	1.75
	High	0.129	5.012
	Combined	0.164	6.265
Plant height	Normal	0.545	5.425
	High	0.752	8.427
	Combined	1.194	13.986
Ear height	Normal	0.647	15.53
	High	0.401	11.219
	Combined	0.612	5.023
Ear length	Normal	0.085	9.534
	High	0.043	5.875
	Combined	-0.028	-0.388
Ear diameter	Normal	0.0067	2.478
	High	0.0114	5.193
	Combined	0.0689	28.32
Number of kernel rows/ear	Normal	0.067	8.049
	High	0.045	6.27
	Combined	-0.495	-64.32
Number of kernels/row	Normal	0.246	12.82
	High	0.254	16.16
	Combined	0.392	22.68
100 kernel weight	Normal	0.116	6.729
	High	0.102	7.597
	Combined	0.127	8.401
Grain yield	Normal	0.39	72.8
	High	0.543	14.50
	Combined	-0.904	-20.08
Moisture % at harvest	Normal	0.061	4.801
	High	0.244	23.56
	Combined	0.374	32.77
Protein	Normal	0.093	14.44
	High	0.114	25.20
	Combined	1.467	-273.80
Tryptophan	Normal	0.001	1.88
	High	0.002	3.75
	Combined	0.117	24.21
Lysine	Normal	0.068	34.44
	High	0.042	25.91
	Combined	0.136	76.34

\*indicates spurious heritability estimates



In the present investigation we obtained higher magnitude of additive variance which revealed that intra-population improvement could be appropriate breeding methodology for open pollinated variety, DQPMC-4(W) to bring about further improvement. Range of full-sib progeny means also indicated scope for selecting full-sibs earlier in maturity and shorter in height.

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